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Fig. 1 (A)

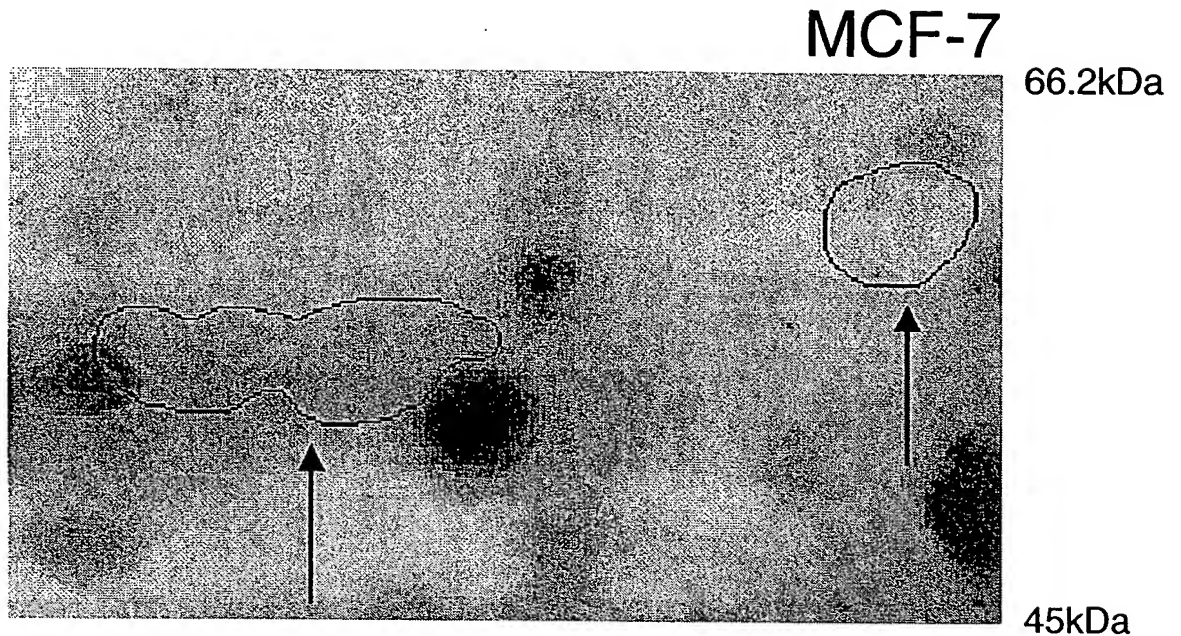
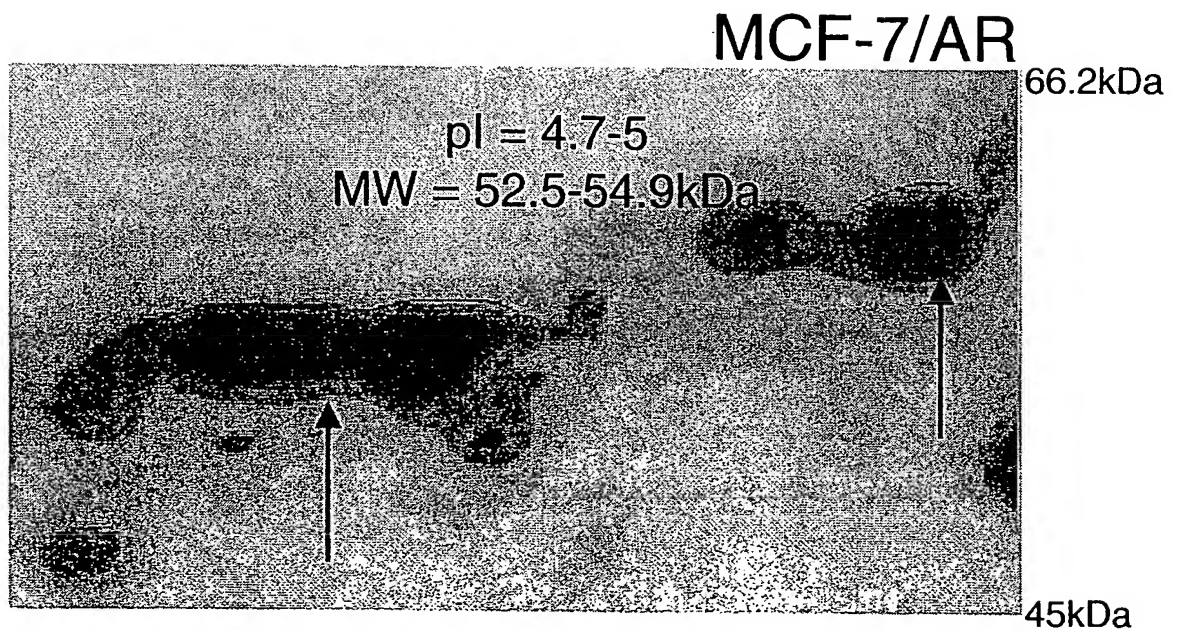


Fig. 1 (B)



~53kDa spot is increased MCF-7/AR

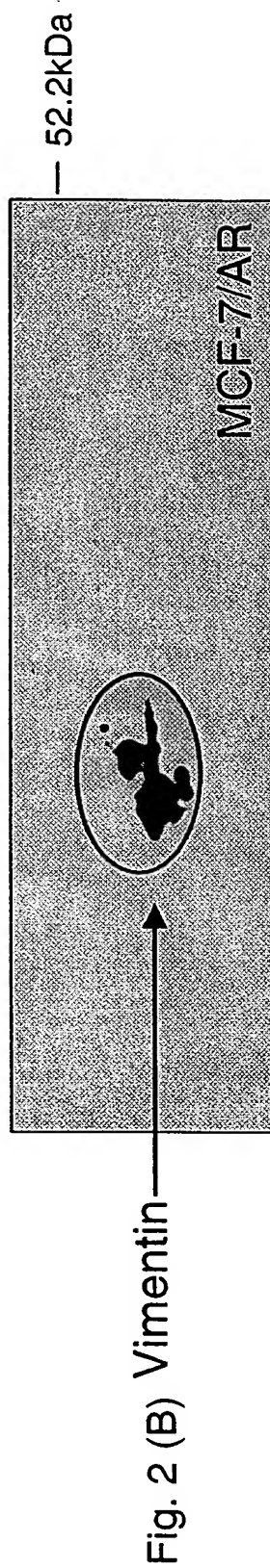
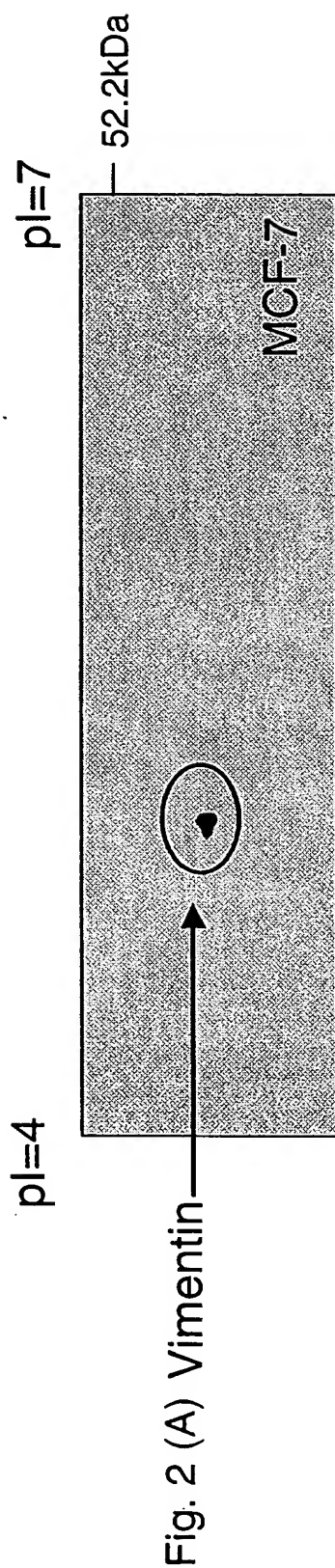


Fig. 3 (A) CEM

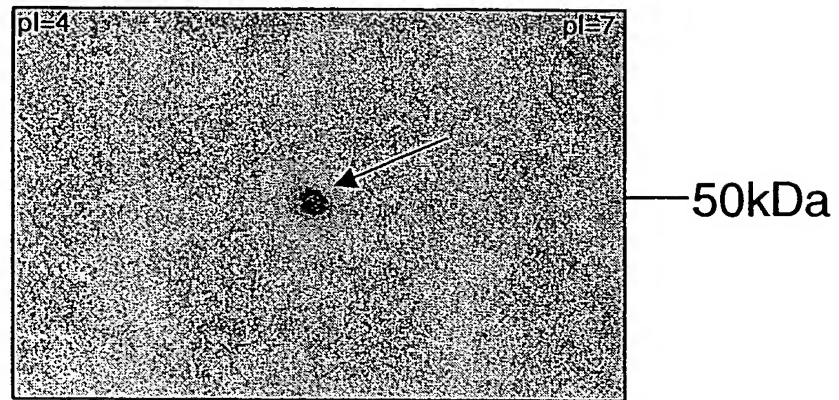


Fig. 3 (B) CEM/VLB

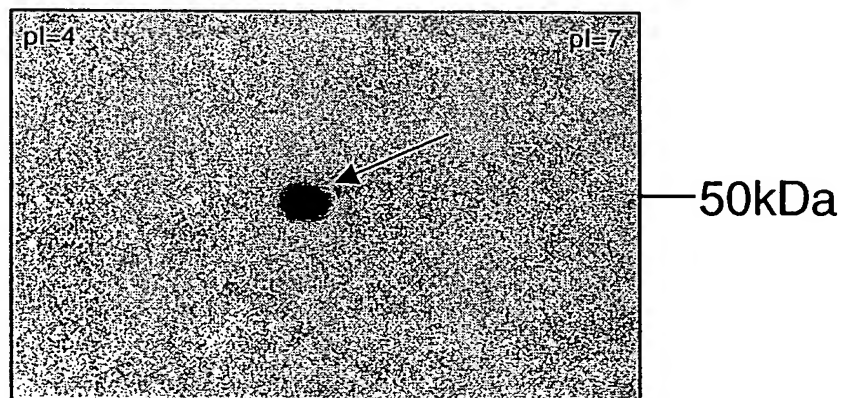


Fig. 4 (A)

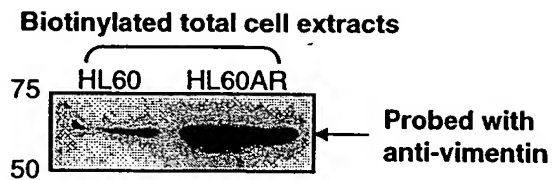


Fig. 4 (B)

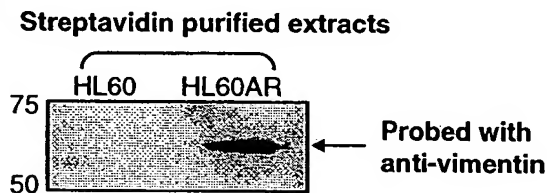


Fig. 4 (C)

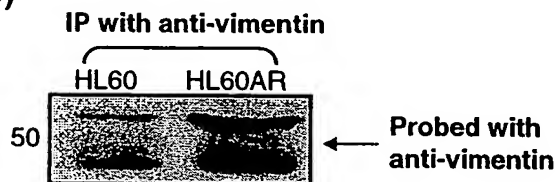


Fig. 4 (D)

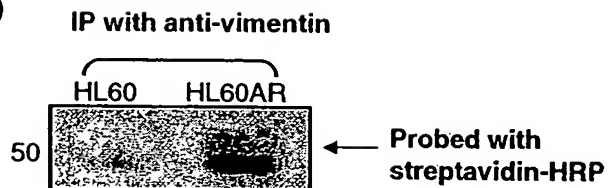


Fig. 5 A

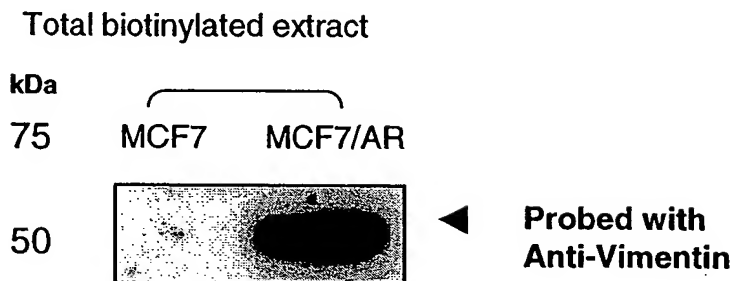


Fig. 5 B

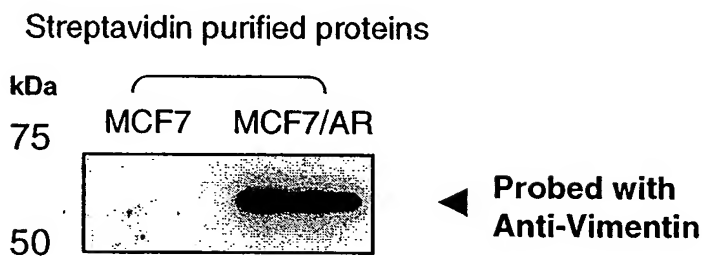


Fig. 5 C

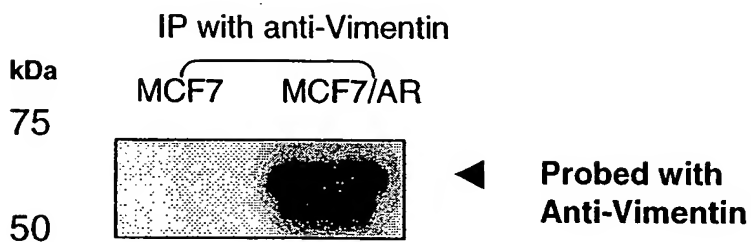
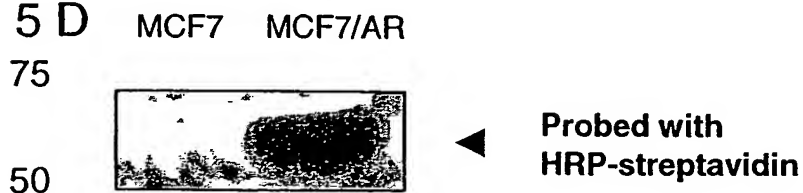


Fig. 5 D



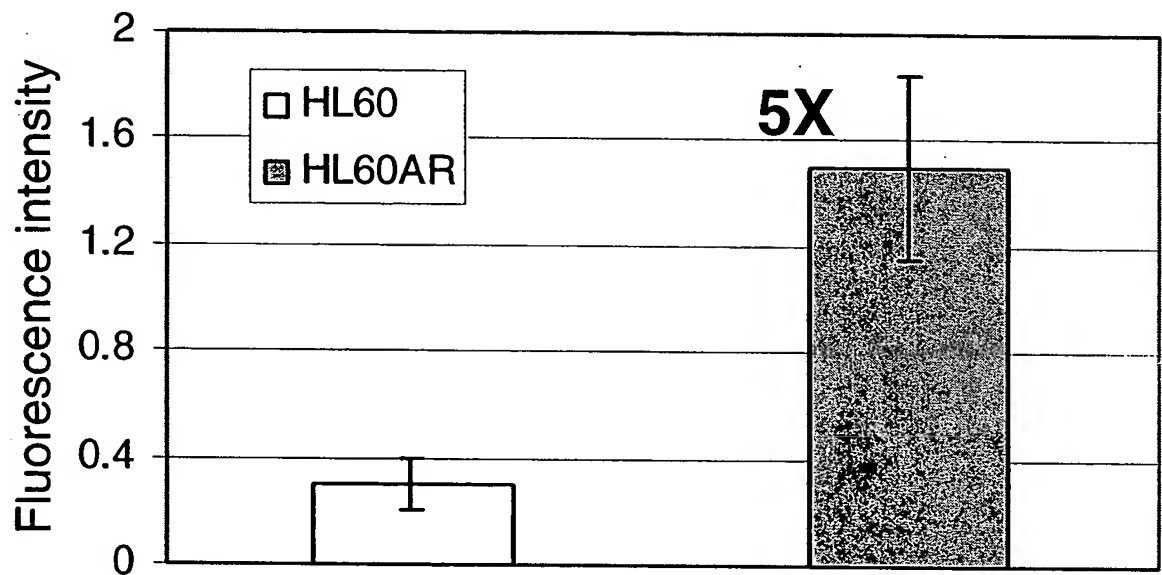


Fig. 6

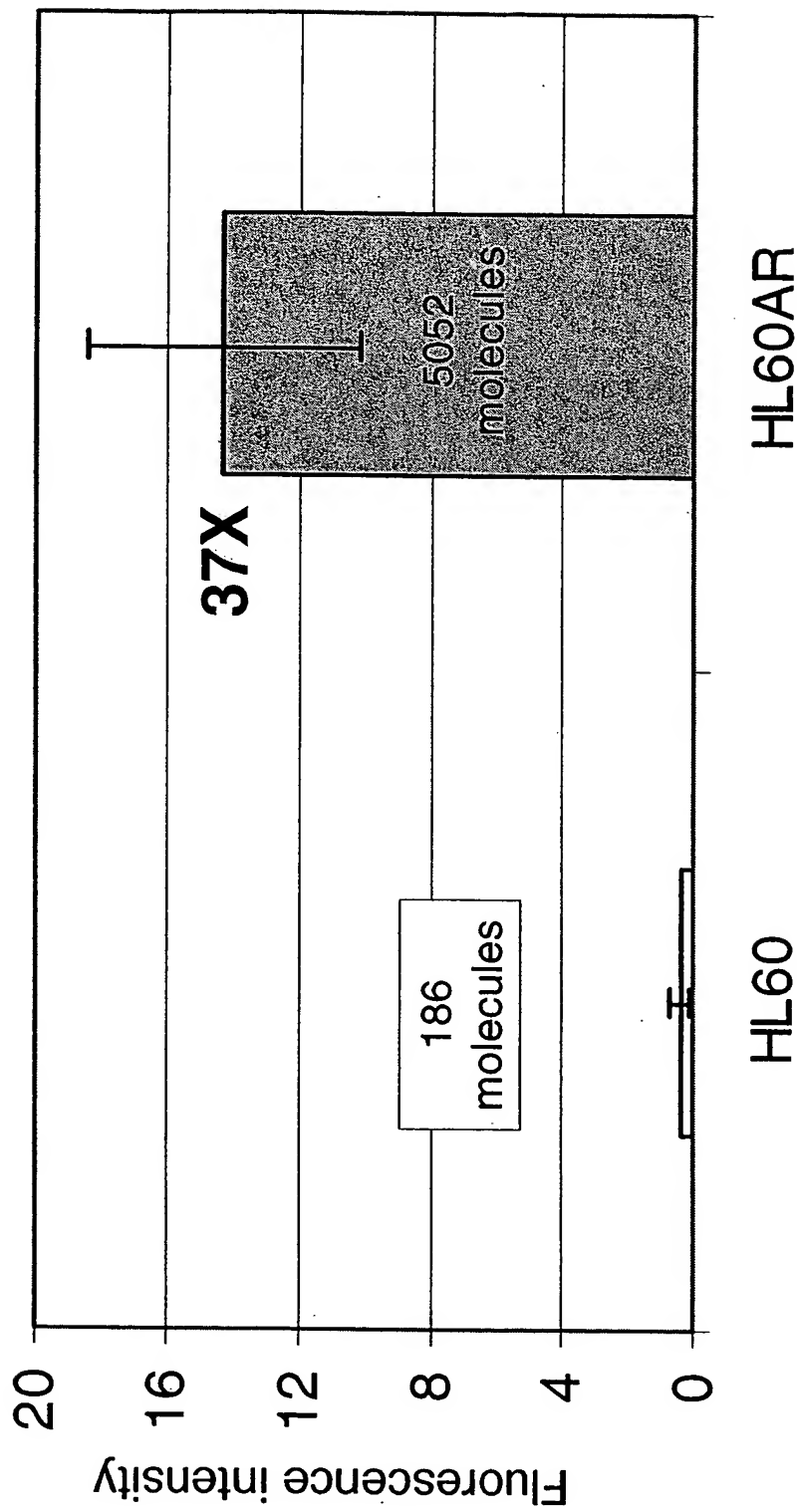


Fig. 7

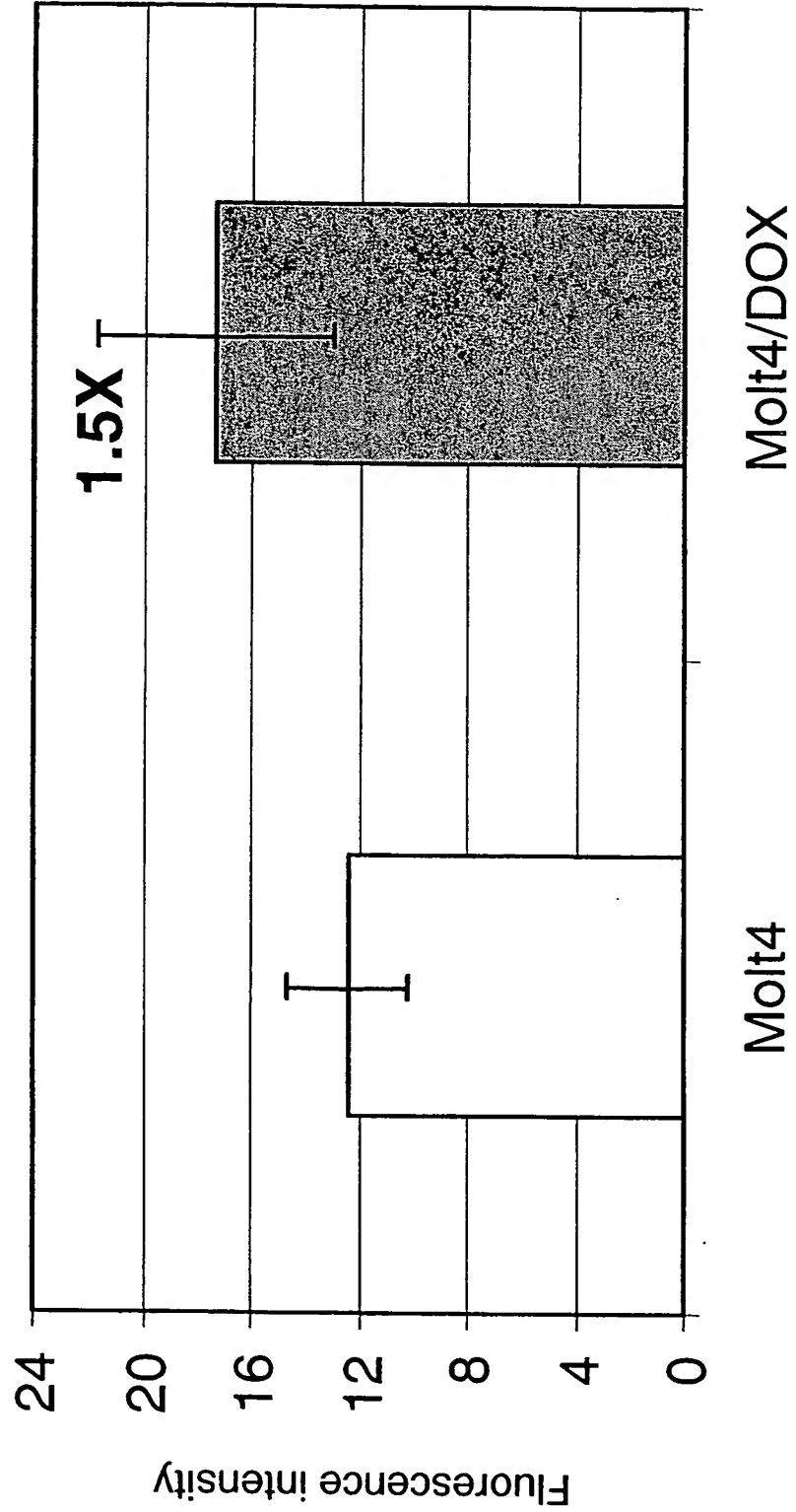


Fig. 8

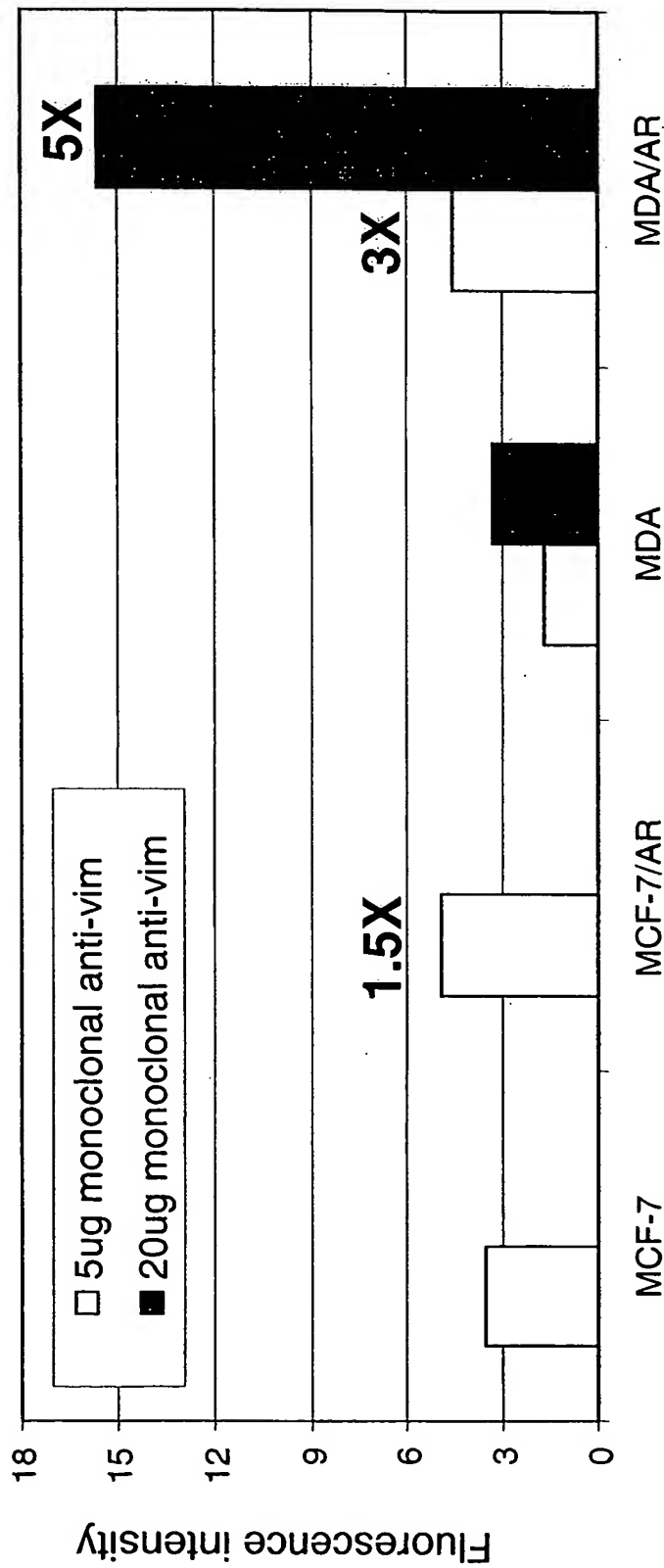


Fig. 9

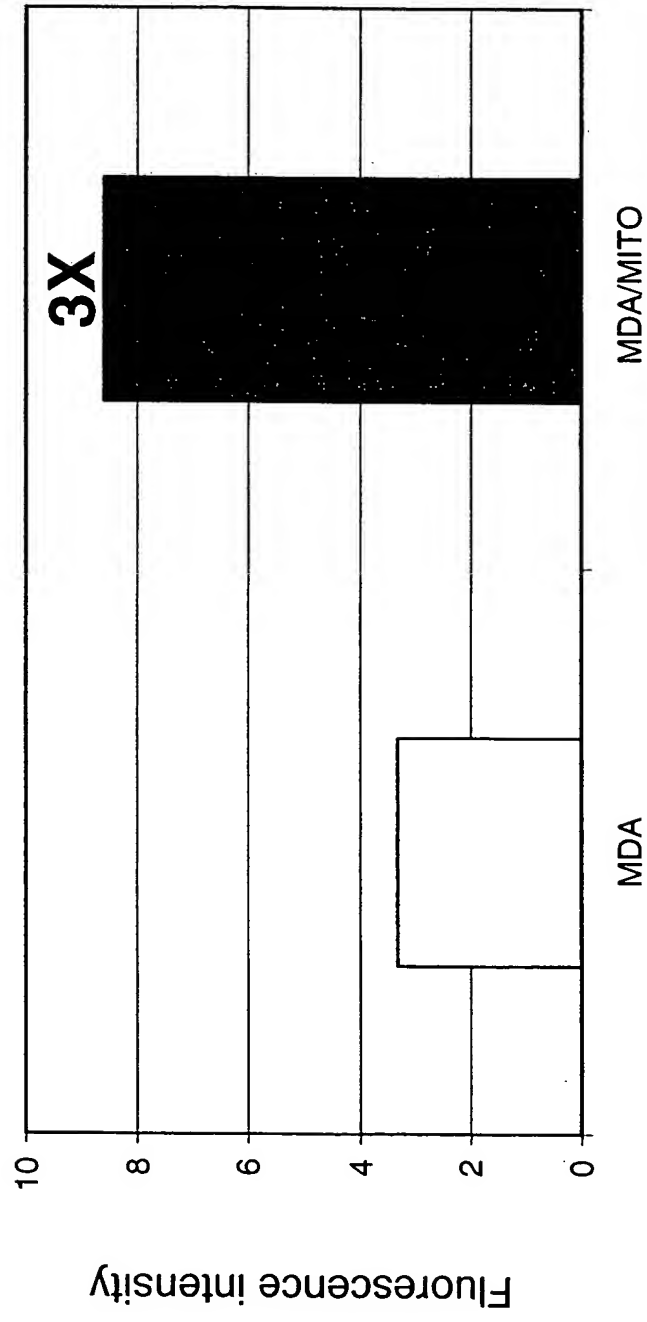


Fig.10

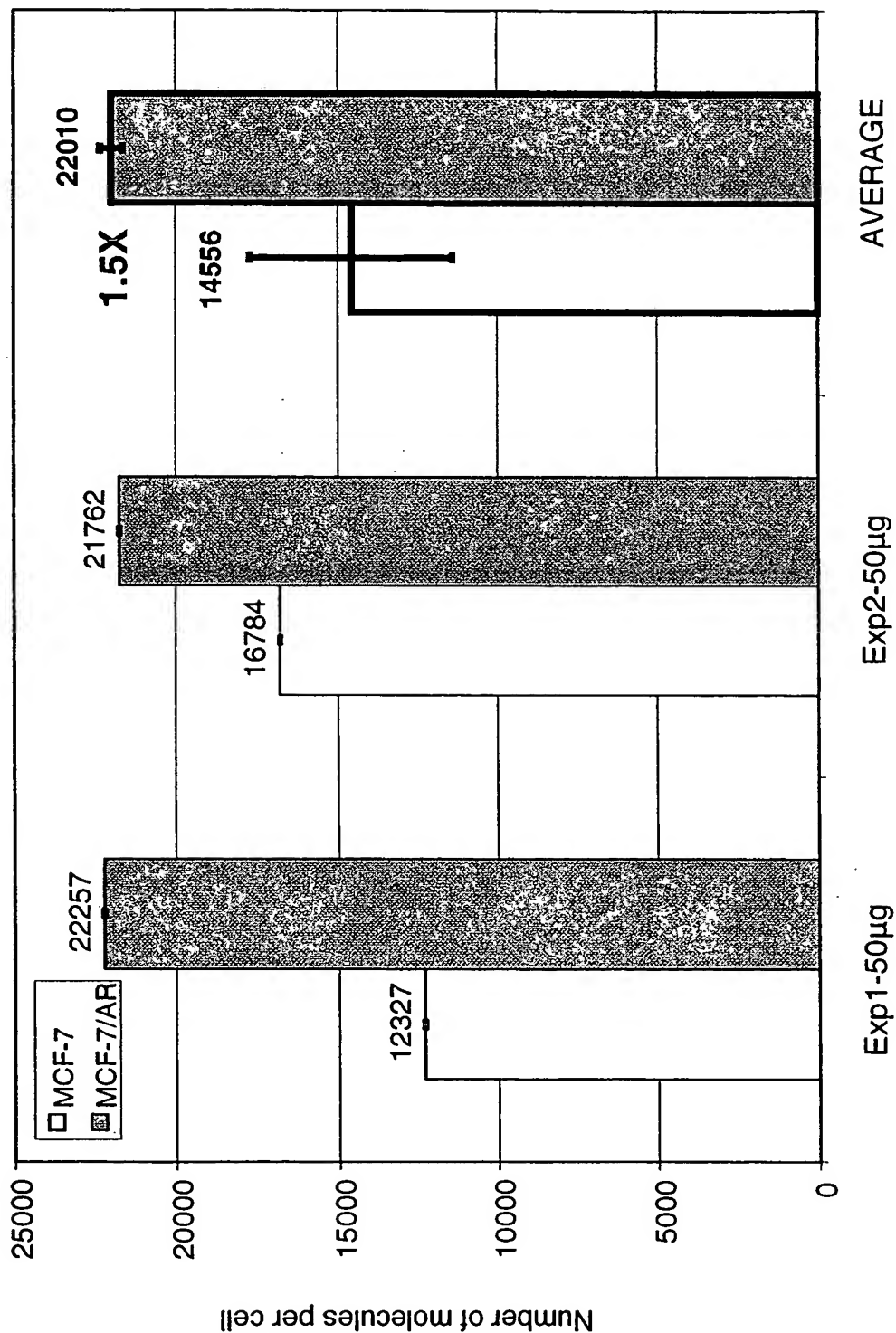


Fig. 11

FIGURE 12

A

POLYPEPTIDE SEQUENCE OF HUMAN VIMENTIN

(GENBANK ACCESSION NO. P08670 (SEQ ID NO.))

```
1  MSTRSVSSSS YRRMFGGPGT ASRPSSRSY VTTSTRTYSL GSALRPSTSR SLYASSPGGV
61  YATRSSAVRL RSSVPGVRL QDSVDFSLAD AINTEFKNTR TNEKVELQEL NDRFANYIDK
121 VRFLEQQNKI LLAELEQLKG QGKSRLGDLY EEEMRELRRQ VDQLTNDKAR VEVERDNLAE
181 DIMRLREKLQ EEMLQREEAE NTLQSFQDV DNASLARLDL ERKVESLQEE IAFLKKLHEE
241 EIQELQAQIQ EQHVQIDVDV SKPDLTAALR DVRQQYESVA AKNLQEAEW YKSKFADLSE
301 AANRNNDALR QAKQESTEYR RQVQSLTCEV DALKGTNESL ERQMREMEEN FAVEAANYQD
361 TIGRLQDEIQ NMKEEMARHL REYQDLLNVK MALDIEIATY RKLLEGEESR ISLPLPNFSS
421 LNLRETNLDS LPLVDTHSKR TFLIKTVETR DGQVINETSQ HHDDLE
```

B

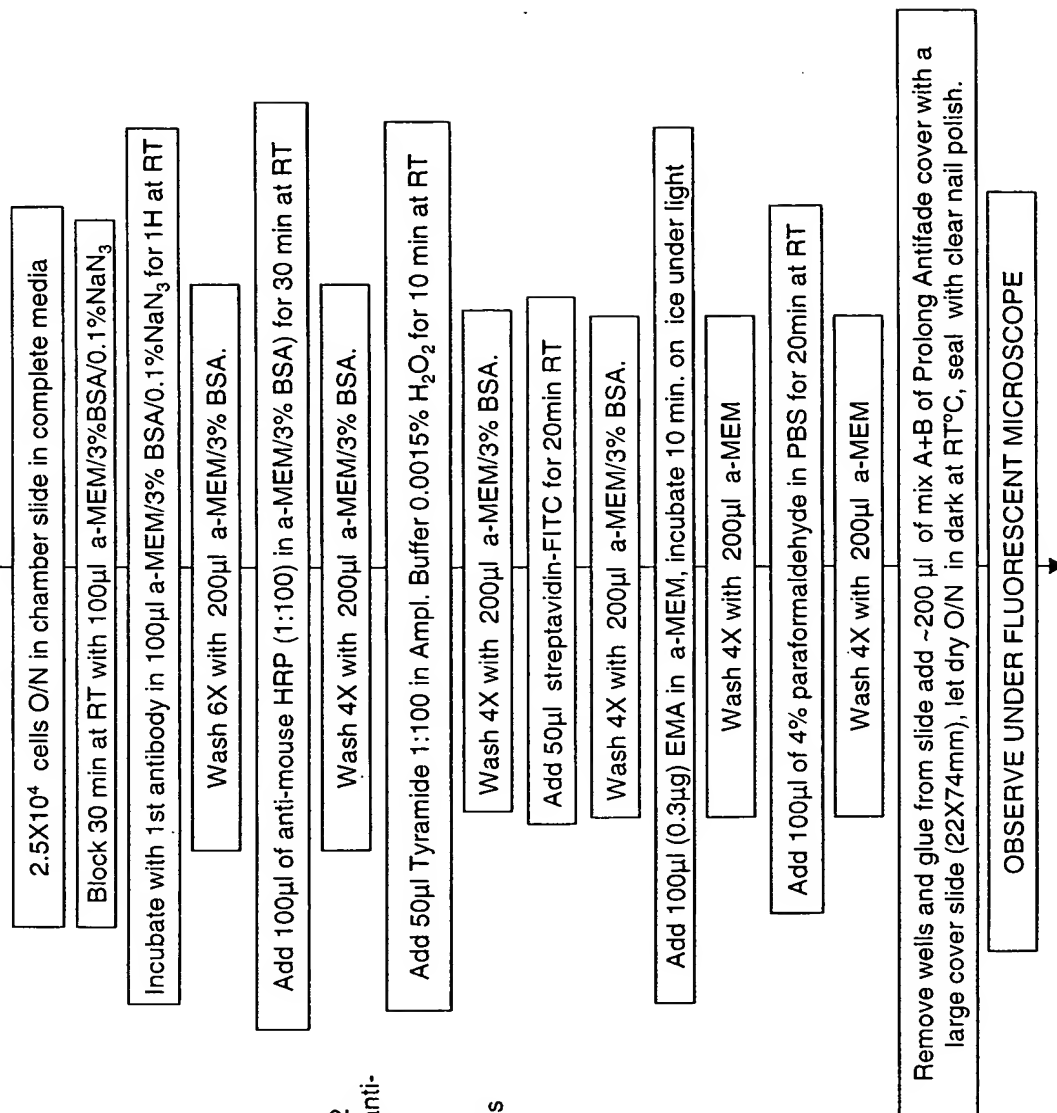
NUCLEIC ACID SEQUENCE OF HUMAN VIMENTIN

(GENBANK ACCESSION NO. X56134 (SEQ ID NO.))

```
1  CGCGCCACCG CCGCCGCCCA GGCCATCGCC ACCCTCCGCA GCCATGTCCA CCAGGTCCGT
61  GTCCTCGTCC TCCTACCGCA GGATGTTTCG CGGCCCGGGC ACCGCGAGCC GGCCGAGCTC
121 CAGCCGGAGC TACGTGACTA CGTCCACCCG CACCTACAGC CTGGGCAGCG CGCTGCGCCC
181 CAGCACCAGC CGCAGCCTCT ACGCCTCGTC CCCGGGCGGC GTGTATGCCA CGCGCTCCTC
241 TGCCGTGCGC CTGCGGAGCA GCGTGCCCGG GGTGCGGCTC CTGCAGGACT CGGTGGACTT
```

301 CTCGCTGGCC GACGCCATCA ACACCGAGTT CAAGAACACC CGCACCAACG AGAAGGTGGA
361 GCTGCAGGAG CTGAATGACC GCTTCGCCAA CTACATCGAC AAGGTGCGCT TCCTGGAGCA
421 GCAGAATAAG ATCCTGCTGG CCGAGCTCGA GCAGCTCAAG GGCCAAGGCA AGTCGCGCCT
481 GGGGGACCTC TACGAGGAGG AGATGCGGGA GCTGCGCCGG CAGGTGGACC AGCTAACCAA
541 CGACAAAGCC CGCGTCGAGG TGGAGCGCGA CAACCTGGCC GAGGACATCA TGCGCCTCCG
601 GGAGAAATTG CAGGAGGAGA TGCTTCAGAG AGAGGAAGCC GAAAACACCC TGCAATCTTT
661 CAGACAGGAT GTTGACAATG CGTCTCTGGC ACGTCTTGAC CTTGAACGCA AAGTGGAATC
721 TTTGCAAGAA GAGATTGCCT TTTTGAAGAA ACTCCACGAA GAGGAAATCC AGGAGCTGCA
781 GGCTCAGATT CAGGAACAGC ATGTCCAAAT CGATGTGGAT GTTTCCAAGC CTGACCTCAC
841 GGCTGCCCTG CGTGACGTAC GTCAGCAATA TGAAAGTGTG GCTGCCAAGA ACCTGCAGGA
901 GGCAGAAGAA TGGTACAAAT CCAAGTTTGC TGACCTCTCT GAGGCTGCCA ACCGGAACAA
961 TGACGCCCTG CGCCAGGCAA AGCAGGAGTC CACTGAGTAC CGGAGACAGG TGCAGTCCCT
1021 CACCTGTGAA GTGGATGCCC TTAAAGGAAC CAATGAGTCC CTGGAACGCC AGATGCGTGA
1081 AATGGAAGAG AACTTTGCCG TTGAAGCTGC TAACTACCAA GACACTATTG GCCGCCTGCA
1141 GGATGAGATT CAGAATATGA AGGAGGAAAT GGCTCGTCAC CTTCGTGAAT ACCAAGACCT
1201 GCTCAATGTT AAGATGGCCC TTGACATTGA GATTGCCACC TACAGGAAGC TGCTGGAAGG
1261 CGAGGAGAGC AGGATTTCTC TGCCTCTTCC AAACTTTTC TCCCTGAACC TGAGGGAAAC
1321 TAATCTGGAT TCACTCCCTC TGGTTGATAC CCACTCAAAA AGGACACTTC TGATTAAGAC
1381 GGTTGAAACT AGAGATGGAC AGGTTATCAA CGAAACTTCT CAGCATCACG ATGACCTTGA
1441 ATAAAAAATTG CACACACTCA GTGCAGCAAT ATATTACCAG CAAGAATAAA AAAGAAATCC
1501 ATATCTTAAA GAAACAGCTT TCAAGTGCCT TTCTGCAGTT TTTCAGGAGC GCAAGATAGA
1561 TTTGGAATAG GAATAAGCTC TAGTTCTTAA CAACCGACAC TCCTACAAGA TTTAGAAAAA
1621 AGTTTACAAC ATAATCTAGT TTACAGAAAA ATCTTGTGCT AGAATACTTT TTAAAAGGTA
1681 TTTTGAATAC CATTAAAACT GCTTTTTTTTT TTCCAGCAAG TATCCAACCA ACTTGGTTCT
1741 GCTTCAATAA ATCTTTGGAA AAACATA

Figure 13A : Procedure for immunofluorescence (non-permeabilized cells)



Amplification kit
 used: TSA kit #2
 with HRP-goat anti-
 mouse IgG and
 Alexa fluor 488
 tyramide from
 molecular probes
 T-20192

Figure 13B: Procedure for immunofluorescence (permeabilized cells)

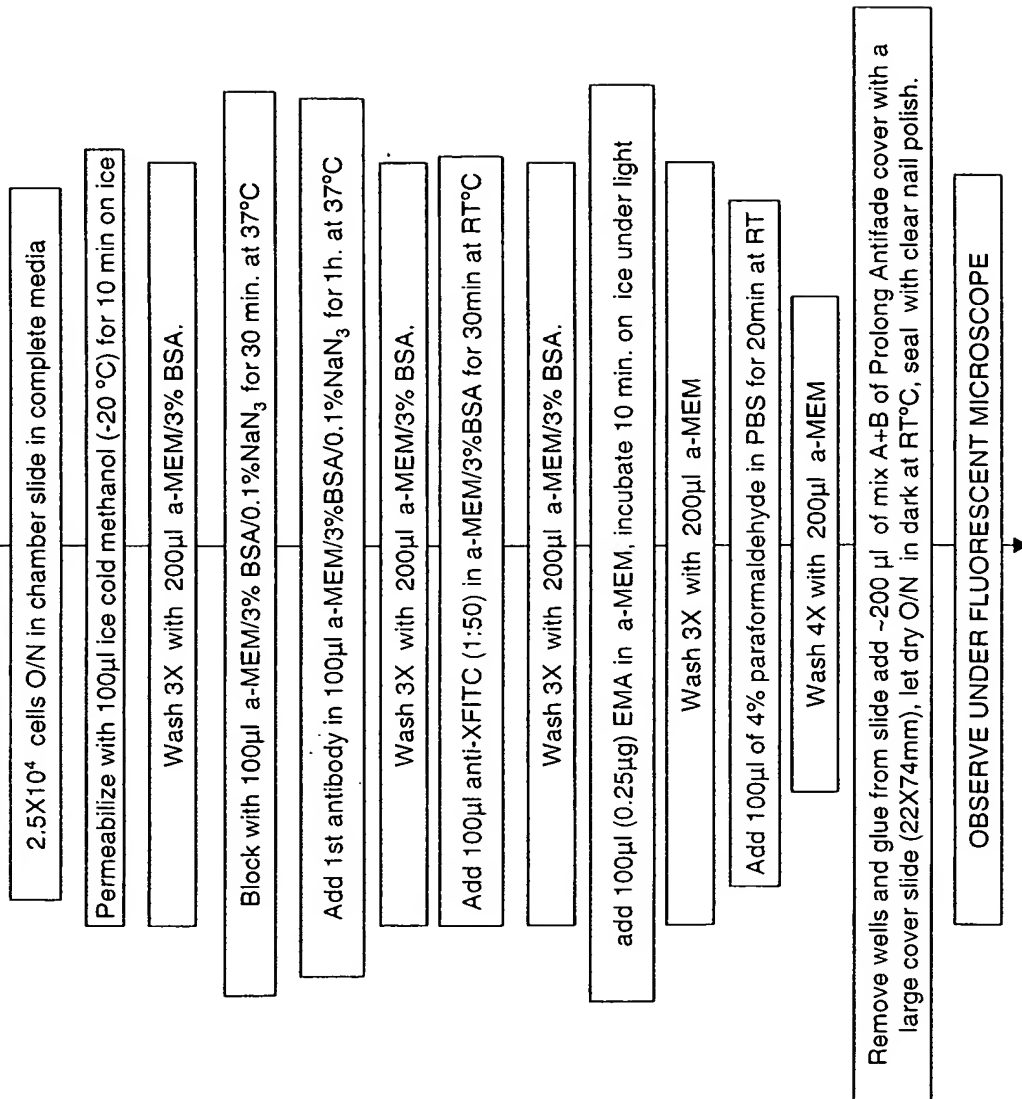


Figure 14

Non
permeabilized

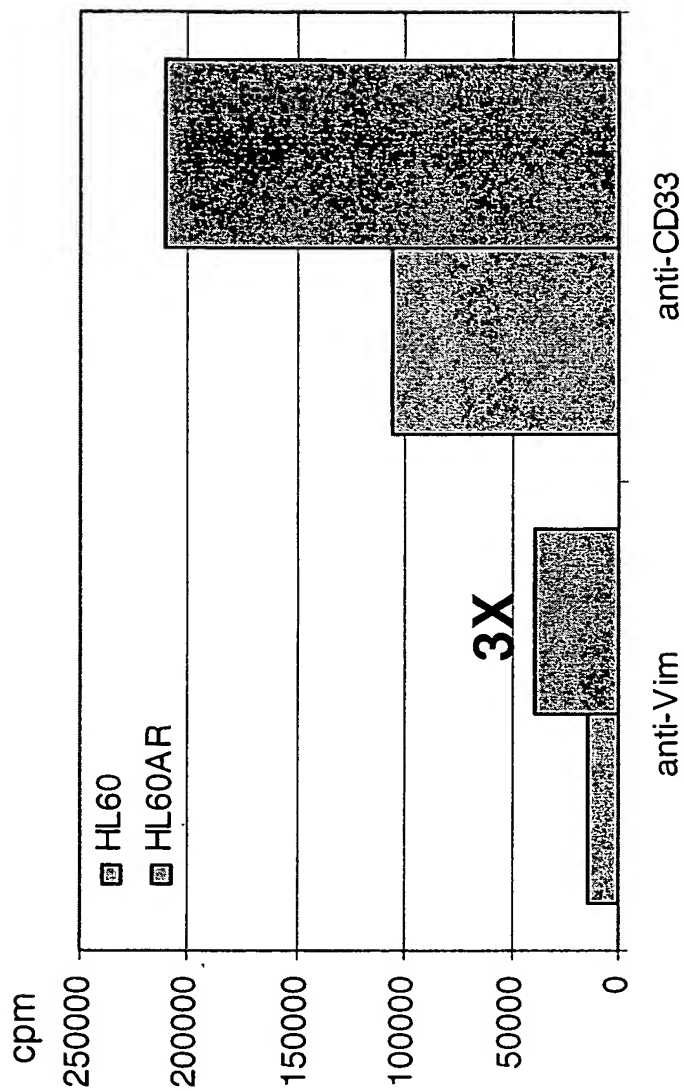
Permeabilized



MCF-7

MCF-7/AR

Figure 15



LS-11-15-03

Figure 16

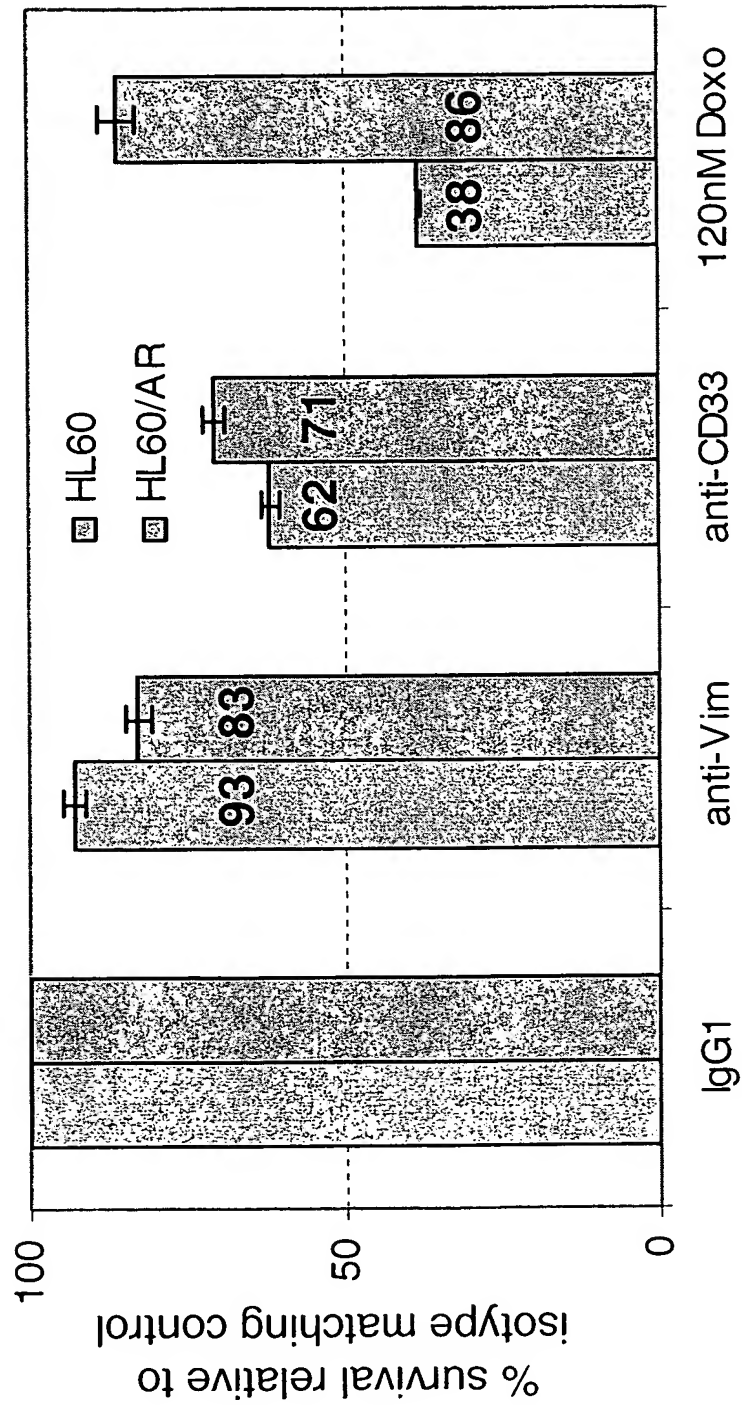
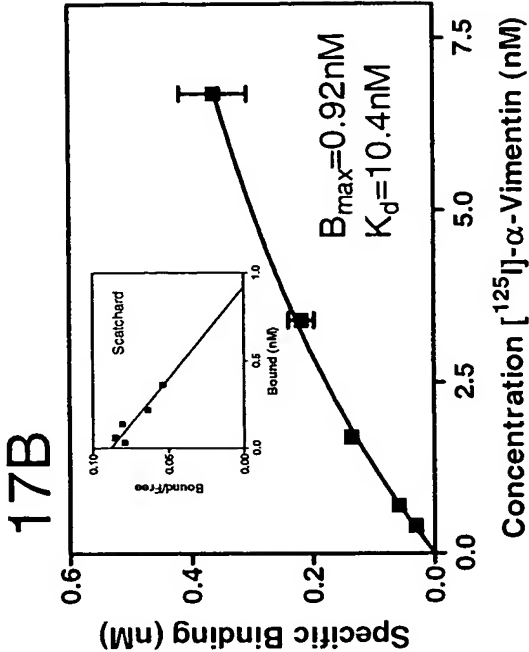


Figure 17



17A

Expt	MDA/ mito (epitopes)	Kd (nM)	r ²
1	2764751	10.4	0.95
2	3477797	5.9	0.97
3	1496035	2.5	0.98
4	2720065	3.2	0.97
5	2012848	6.7	0.97
Ave	2494299	5.7	
Std	761530	3.1	

17C

cells	AVE	STD	Kd	R/S
MCF-7	9.1.E+03	8.8.E+03	nd	
MCF-7/AR	3.8.E+05	1.1.E+05	nd	41.2
MDA	6.3.E+05	1.6.E+05	9.3 ± 2.8	
MDA/ mito	2.5.E+06	7.6.E+05	5.7 ± 3.1	4.0
SKOV3	7.4.E+05	3.7.E+05	nd	
SKOV/T320	1.2.E+06	2.0.E+05	nd	1.6
2008	4.1.E+04	2.2.E+04	nd	
2008/T320	8.3.E+04	1.3.E+04	nd	2.0

Figure 18

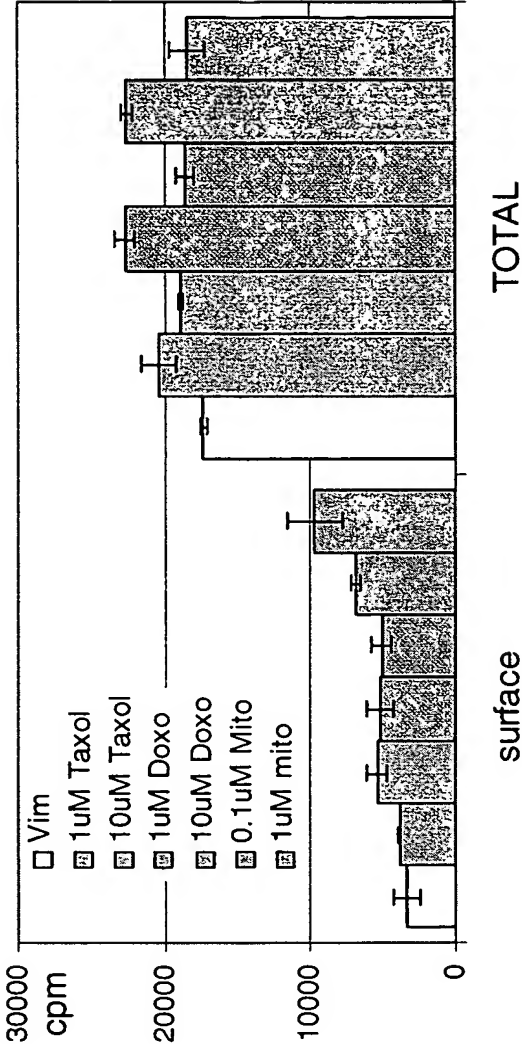


Figure 19

